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**Short Bio**

I received a PhD in Medicine from the University of Amsterdam in 1995 (advisor Prof. Jaap Goudsmit). For several years I split my time between the Department of Microbiology at the University of Amsterdam and the Theoretical Biology and Biophysics Group at the Los Alamos National Laboratory. In addition, I spent some time at the Australian National University (ANU) with Prof. Adrian Gibbs. In 1996 I became a full-time postdoc at LANL, then a staff scientist at the [HIV Database and Analysis Project](#) in 1999. In 2002 NIAID agreed to fund a new sequence and immunology database for [hepatitis C virus](#), which was subsumed into the Viral Bioinformatics Resource Center in 2007 – only to be moved again into the [Viral Pathogen Research \(ViPR\) database](#) when the number of BRCs was reduced to five in 2009. In 2009 a database for [Hemorrhagic Fever Viruses](#) was started, funded by the Department of Defense.

**Research Interests**

With a strong background in molecular epidemiology, my work currently focuses on making sequence data more easily accessible for researchers. This involves storing and curating them (automatically as much as possible) and creating tools and interfaces to retrieve and analyze the sequences. The early “HIV database” consisted of a number of sequences in fasta format that were distributed in printed form and on CDs. From this starting point the database project built several generations of databases and interfaces, as well as an extensive tool suite to manipulate and analyze the sequences. The HCV and HFV databases were natural candidates for a very similar approach. A multi-virus (multi-viral family) database will need to rely on well-annotated reference sequences to achieve the same functionality as the single-organism HIV database. From this came my involvement in the annotation of NCBI’s RefSeq database, worldwide efforts to create automated viral annotation pipelines, and efforts to organize viral sequence information in the form of the viral Gene Ontology (GO), the Genomic Standards Consortium (GSC), and the International Committee for the Taxonomy of Viruses (ICTV), and am a member of the ViPR scientific advisory board.